

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/526,569
Source: PCT
Date Processed by STIC: 3-13-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses.

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - cPAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER

10/526/569

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .5; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Missigned Amino Numbering The numbering under each 3rd amino acid is missigned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(1) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(2) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(3) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences.

8 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <211> Response

Per 1.823 of Sequence Rules, the only valid <211> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <211> response is Unknown or Artificial Sequence.

11 Use of <220>

Sequence(s) missing the <220> feature and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <211> "Organism" response is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (See 1.823 of Sequence Rules)

12 PatentIn 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa

"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

RAW SEQUENCE LISTING

DATE: 03/13/2005

PATENT APPLICATION: US/10/526,569

TIME: 12:11:40

Input Set : A:\200521 SEQ LIST.txt

Output Set: N:\CRF4\03132005\J526569.raw

3 <110> APPLICANT: Yoshihiro OHMIYA, EMIKO ASHIDAKA and Seiji ITO
 5 <120> TITLE OF INVENTION: Secreted or membrane-binding chimeric protein
 7 <130> FILE REFERENCE: 200521/US
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/526,569
 C--> 9 <141> CURRENT FILING DATE: 2005-03-04
 9 <160> NUMBER OF SEQ ID NOS: 10
 11 <170> SOFTWARE: PatentIn version 3.1
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 2388
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Artificial Sequence
 18 <220> FEATURE:
 19 <223> OTHER INFORMATION: fused gene consisting of Vargula Luciferase, yellow
 fluorescence
 20 protein from Aequorea and a DNA coding for spacer peptide
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (1)..(2388)
 26 <400> SEQUENCE: 1
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 28 Met Lys Ile Ile Ile Leu Ser Val Ile Leu Ala Tyr Cys Val Thr Asp
 29 1 5 10 15
 31 aac tgt caa gat gca tgt cct gta gaa gcg gaa ccg cca tca agt aca 96
 32 Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Pro Pro Ser Ser Thr
 33 20 25 30
 35 cca aca gtt cca act tct tgt gaa gct aaa gaa gga gaa tgt ata gat 144
 36 Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp
 37 35 40 45
 39 acc aga tgc gca aca tgt aaa cga gat ata cta tca gat gga ctg tgt 192
 40 Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys
 41 50 55 60
 43 gaa aat aaa cca ggg aag aca tgc tgt aga atg tgc cag tat gtg att 240
 44 Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile
 45 65 70 75 80
 47 gaa tgc aga gta gaa gca gct ggt tat ttt aga acg ttt tac ggc aaa 288
 48 Glu Cys Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Gly Lys
 49 85 90 95
 51 aga ttt aat ttt cag gaa cct ggt aaa tat gtg ctg gct agg gga acc 336
 52 Arg Phe Asn Phe Gln Glu Pro Gly Lys Tyr Val Leu Ala Arg Gly Thr
 53 100 105 110
 55 aag ggt ggc gat tgg tct gta acc ctc acc atg gag aat cta gat gga 384
 56 Lys Gly Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly
 57 115 120 125
 59 cag aag gga gct gtg ctg act aag aca aca ctg gag gtt gca gga gac 432

Does Not Comply
 Corrected Diskette Needed
 (pg. 4)

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/526,569

DATE: 03/13/2005

TIME: 12:11:40

Input Set : A:\200521 SEQ LIST.txt

Output Set: N:\CRF4\03132005\J526569.raw

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60 Gln Lys Gly Ala Val Leu Thr Lys Thr Thr Leu Glu Val Ala Gly Asp
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63 gta ata gac att act caa gct act gca gat cct atc aca gtt aac gga      480
64 Val Ile Asp Ile Thr Gln Ala Thr Ala Asp Pro Ile Thr Val Asn Gly
65 145                      150                      155                      160
67 gga gct gac cca gtt atc gct aac ccg ttc aca att ggt gag gtg acc      528
68 Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr
69                      165                      170                      175
71 att gct gtt gtt gaa ata ccg ggc ttc aat atc aca gtc atc gaa ttc      576
72 Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe
73                      180                      185                      190
75 ttt aaa cta atc gtg att gat att ctg gga gga aga tct gtg aga att      624
76 Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile
77      195                      200                      205
79 gct cca gac aca gca aac aaa gga ctg ata tct ggt atc tgt ggt aat      672
80 Ala Pro Asp Thr Ala Asn Lys Gly Leu Ile Ser Gly Ile Cys Gly Asn
81      210                      215                      220
83 ctg gag atg aat gac gct gat gac ttt act aca gat gca gat cag ctg      720
84 Leu Glu Met Asn Asp Ala Asp Asp Phe Thr Thr Asp Ala Asp Gln Leu
85 225                      230                      235                      240
87 gcg atc caa ccc aac ata aac aaa gag ttc gac ggc tgc cca ttc tat      768
88 Ala Ile Gln Pro Asn Ile Asn Lys Glu Phe Asp Gly Cys Pro Phe Tyr
89                      245                      250                      255
91 ggc aat cct tct gat atc gaa tac tgc aaa ggt ctg atg gag cca tac      816
92 Gly Asn Pro Ser Asp Ile Glu Tyr Cys Lys Gly Leu Met Glu Pro Tyr
93                      260                      265                      270
95 aga gct gta tgt cgt aac aat atc aac ttc tac tat tac act cta tcc      864
96 Arg Ala Val Cys Arg Asn Asn Ile Asn Phe Tyr Tyr Tyr Thr Leu Ser
97      275                      280                      285
99 tgt gcc ttc gct tac tgt atg gga gga gaa gaa aga gct aaa cac gtc      912
100 Cys Ala Phe Ala Tyr Cys Met Gly Gly Glu Glu Arg Ala Lys His Val
101      290                      295                      300
103 ctt ttc gac tat gtt gag aca tgc gct gcg ccg gaa acg aga gga acg      960
104 Leu Phe Asp Tyr Val Glu Thr Cys Ala Ala Pro Glu Thr Arg Gly Thr
105 305                      310                      315                      320
107 tgt gtt tta tca gga cat act ttc tat gac aca ttc gac aaa gca aga      1008
108 Cys Val Leu Ser Gly His Thr Phe Tyr Asp Thr Phe Asp Lys Ala Arg
109                      325                      330                      335
111 tat caa ttc cag ggc cca tgc aag gag att ctg atg gcc gca gac tgt      1056
112 Tyr Gln Phe Gln Gly Pro Cys Lys Glu Ile Leu Met Ala Ala Asp Cys
113                      340                      345                      350
115 tac tgg aac aca tgg gat gta aag gtt tca cat aga gac gtc gaa tca      1104
116 Tyr Trp Asn Thr Trp Asp Val Lys Val Ser His Arg Asp Val Glu Ser
117                      355                      360                      365
119 tac act gag gta gag aaa gta aca atc agg aaa cag tca act gta gta      1152
120 Tyr Thr Glu Val Glu Lys Val Thr Ile Arg Lys Gln Ser Thr Val Val
121      370                      375                      380
123 gat ctc att gtg gat ggc aag cag gtc aag gtt gga gga gtg gat gta      1200
124 Asp Leu Ile Val Asp Gly Lys Gln Val Lys Val Gly Gly Val Asp Val

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Input Set : A:\200521 SEQ LIST.txt

Output Set: N:\CRF4\03132005\J526569.raw

125	385		390		395		400	
127	tct atc ccg tac agc	tct gag aac act tcc ata tac tgg cag gat gga	1248					
128	Ser Ile Pro Tyr Ser	Glu Asn Thr Ser Ile Tyr Trp Gln Asp Gly						
129		405 410 415						
131	gac atc ctg acg acg gcc atc cta cct gaa gct ctt gtc gtt aag ttc	1296						
132	Asp Ile Leu Thr Thr Ala Ile Leu Pro Glu Ala Leu Val Val Lys Phe							
133		420 425 430						
135	aac ttt aag cag ctc ctt gta gtt cat atc aga gat cca ttc gat gga	1344						
136	Asn Phe Lys Gln Leu Leu Val Val His Ile Arg Asp Pro Phe Asp Gly							
137		435 440 445						
139	aag aca tgc ggc ata tgt ggt aac tat aat caa gat tca act gat gat	1392						
140	Lys Thr Cys Gly Ile Cys Gly Asn Tyr Asn Gln Asp Ser Thr Asp Asp							
141		450 455 460						
143	ttc ttt gac gca gaa gga gca tgc gct cta acc ccc aac ccc cca gga	1440						
144	Phe Phe Asp Ala Glu Gly Ala Cys Ala Leu Thr Pro Asn Pro Pro Gly							
145	465	470 475 480						
147	tgt aca gag gaa cag aaa cca gaa gct gag cga ctt tgc aat aat ctc	1488						
148	Cys Thr Glu Glu Gln Lys Pro Glu Ala Glu Arg Leu Cys Asn Asn Leu							
149		485 490 495						
151	ttt gat tct tct atc gac gag aaa tgt aat gtc tgc tac aag cct gac	1536						
152	Phe Asp Ser Ser Ile Asp Glu Lys Cys Asn Val Cys Tyr Lys Pro Asp							
153		500 505 510						
155	cgg att gcc cga tgt atg tac gag tat tgc ctg agg gga caa caa gga	1584						
156	Arg Ile Ala Arg Cys Met Tyr Glu Tyr Cys Leu Arg Gly Gln Gln Gly							
157		515 520 525						
159	ttt tgt gac cat gct tgg gag ttc aag aaa gaa tgc tac ata aaa cat	1632						
160	Phe Cys Asp His Ala Trp Glu Phe Lys Lys Glu Cys Tyr Ile Lys His							
161		530 535 540						
163	gga gac act cta gaa gta cca cct gaa tgt caa gga tcc gtg agc aag	1680						
164	Gly Asp Thr Leu Glu Val Pro Pro Glu Cys Gln Gly Ser Val Ser Lys							
165	545	550 555 560						
167	ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac	1728						
168	Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp							
169		565 570 575						
171	ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc	1776						
172	Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly							
173		580 585 590						
175	gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc	1824						
176	Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly							
177		595 600 605						
179	aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc	1872						
180	Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly							
181		610 615 620						
183	ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cag cac gac ttc	1920						
184	Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe							
185	625	630 635 640						
187	ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc	1968						
188	Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe							
189		645 650 655						

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Input Set : A:\200521 SEQ LIST.txt

Output Set: N:\CRF4\03132005\J526569.raw

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191 ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag      2016
192 Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
193      660      665      670
195 ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag      2064
196 Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
197      675      680      685
199 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc      2112
200 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
201      690      695      700
203 cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg      2160
204 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
205 705      710      715      720
207 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc      2208
208 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
209      725      730      735
211 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg      2256
212 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
213      740      745      750
215 ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc      2304
216 Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
217      755      760      765
219 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc      2352
220 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
221      770      775      780
223 ggg atc act ctc ggc atg gac gag ctg tac aag taa      2388
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225 785      790      795
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228 <211> LENGTH: 2502
229 <212> TYPE: DNA
230 <213> ORGANISM: chimeric protein
232 <220> FEATURE:
233 <221> NAME/KEY: CDS
234 <222> LOCATION: (1)..(2502)
236 <400> SEQUENCE: 2
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238 Met Lys Ile Ile Ile Leu Ser Val Ile Leu Ala Tyr Cys Val Thr Asp
239 1      5      10      15
241 aac tgt caa gat gca tgt cct gta gaa gcg gaa ccg cca tca agt aca      96
242 Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Pro Pro Ser Ser Thr
243      20      25      30
245 cca aca gtt cca act tct tgt gaa gct aaa gaa gga gaa tgt ata gat      144
246 Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp
247      35      40      45
249 acc aga tgc gca aca tgt aaa cga gat ata cta tca gat gga ctg tgt      192
250 Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys
251      50      55      60
253 gaa aat aaa cca ggg aag aca tgc tgt aga atg tgc cag tat gtg att      240
254 Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile

```

Invalid
ResponseMandatory
CAS Organism response
has to be either
Artificial
UnknownOR
Genus/
Species.
See item#10 on
error
summary
sheet.
3/13/05The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
occurrences for similar errors.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/526,569

DATE: 03/13/2005

TIME: 12:11:40

Input Set : A:\200521 SEQ LIST.txt

Output Set: N:\CRF4\03132005\J526569.raw

255	65	70	75	80	
257	gaa tgc aga gta gaa gca gct ggt tat ttt aga acg ttt tac ggc aaa				288
258	Glu Cys Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Gly Lys				
259		85	90	95	
261	aga ttt aat ttt cag gaa cct ggt aaa tat gtg ctg gct agg gga acc				336
262	Arg Phe Asn Phe Gln Glu Pro Gly Lys Tyr Val Leu Ala Arg Gly Thr				
263		100	105	110	
265	aag ggt ggc gat tgg tct gta acc ctc acc atg gag aat cta gat gga				384
266	Lys Gly Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly				
267		115	120	125	
269	cag aag gga gct gtg ctg act aag aca aca ctg gag gtt gca gga gac				432
270	Gln Lys Gly Ala Val Leu Thr Lys Thr Thr Leu Glu Val Ala Gly Asp				
271		130	135	140	
273	gta ata gac att act caa gct act gca gat cct atc aca gtt aac gga				480
274	Val Ile Asp Ile Thr Gln Ala Thr Ala Asp Pro Ile Thr Val Asn Gly				
275	145	150	155	160	
277	gga gct gac cca gtt atc gct aac ccg ttc aca att ggt gag gtg acc				528
278	Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr				
279		165	170	175	
281	att gct gtt gtt gaa ata ccg ggc ttc aat atc aca gtc atc gaa ttc				576
282	Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe				
283		180	185	190	
285	ttt aaa cta atc gtg att gat att ctg gga gga aga tct gtg aga att				624
286	Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile				
287		195	200	205	
289	gct cca gac aca gca aac aaa gga ctg ata tct ggt atc tgt ggt aat				672
290	Ala Pro Asp Thr Ala Asn Lys Gly Leu Ile Ser Gly Ile Cys Gly Asn				
291		210	215	220	
293	ctg gag atg aat gac gct gat gac ttt act aca gat gca gat cag ctg				720
294	Leu Glu Met Asn Asp Ala Asp Asp Phe Thr Thr Asp Ala Asp Gln Leu				
295	225	230	235	240	
297	gcg atc caa ccc aac ata aac aaa gag ttc gac ggc tgc cca ttc tat				768
298	Ala Ile Gln Pro Asn Ile Asn Lys Glu Phe Asp Gly Cys Pro Phe Tyr				
299		245	250	255	
301	ggc aat cct tct gat atc gaa tac tgc aaa ggt ctg atg gag cca tac				816
302	Gly Asn Pro Ser Asp Ile Glu Tyr Cys Lys Gly Leu Met Glu Pro Tyr				
303		260	265	270	
305	aga gct gta tgt cgt aac aat atc aac ttc tac tat tac act cta tcc				864
306	Arg Ala Val Cys Arg Asn Asn Ile Asn Phe Tyr Tyr Tyr Thr Leu Ser				
307		275	280	285	
309	tgt gcc ttc gct tac tgt atg gga gga gaa gaa aga gct aaa cac gtc				912
310	Cys Ala Phe Ala Tyr Cys Met Gly Gly Glu Glu Arg Ala Lys His Val				
311		290	295	300	
313	ctt ttc gac tat gtt gag aca tgc gct gcg ccg gaa acg aga gga acg				960
314	Leu Phe Asp Tyr Val Glu Thr Cys Ala Ala Pro Glu Thr Arg Gly Thr				
315	305	310	315	320	
317	tgt gtt tta tca gga cat act ttc tat gac aca ttc gac aaa gca aga				1008
318	Cys Val Leu Ser Gly His Thr Phe Tyr Asp Thr Phe Asp Lys Ala Arg				
319		325	330	335	

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/526,569

DATE: 03/13/2005

TIME: 12:11:41

Input Set : A:\200521 SEQ LIST.txt

Output Set: N:\CRF4\03132005\J526569.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date